



OIPE

## RAW SEQUENCE LISTING

DATE: 05/21/2002

PATENT APPLICATION: US/10/039,876A

TIME: 10:05:35

Input Set : A:\97-63C1 SEQ.txt

Output Set: N:\CRF3\05212002\J039876A.raw

**ENTERED**

3 <110> APPLICANT: Conklin, Darrell C.  
 4 Blumberg, Hal  
 8 <120> TITLE OF INVENTION: A HUMAN 2-19 PROTEIN HOMOLOGUE, Z219A  
 11 <130> FILE REFERENCE: 97-63C1  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/039,876A  
 C--> 13 <141> CURRENT FILING DATE: 2001-10-26  
 13 <150> PRIOR APPLICATION NUMBER: US 60/061,712  
 14 <151> PRIOR FILING DATE: 1997-10-06  
 16 <150> PRIOR APPLICATION NUMBER: US 09/167,513  
 17 <151> PRIOR FILING DATE: 1998-10-06  
 19 <160> NUMBER OF SEQ ID NOS: 28  
 21 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 876  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Homo sapiens  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (119)...(823)  
 32 <400> SEQUENCE: 1

33	gcccgcacct gcccgcacacg accgctgccc gccccttgcc ttccctgaccc agggggtccg	60
34	ctggctgcgg tcgcttgga gctgccgcca gggccaggag gggagcggca cctggaag	118
35	atg cgc cca ttg gct ggt ggc ctg ctc aag gtg gtg ttc gtg gtc ttc	166
36	Met Arg Pro Leu Ala Gly Gly Leu Leu Lys Val Val Phe Val Val Phe	
37	1 5 10 15	
39	gcc tcc ttg tgt gcc tgg tat tgc ggg tac ctg ctc gca gag ctc att	214
40	Ala Ser Leu Cys Ala Trp Tyr Ser Gly Tyr Leu Leu Ala Glu Leu Ile	
41	20 25 30	
43	cca gat gca ccc ctg tcc agt gct gcc tat agc atc cgc agc atc ggg	262
44	Pro Asp Ala Pro Leu Ser Ser Ala Ala Tyr Ser Ile Arg Ser Ile Gly	
45	35 40 45	
47	gag agg cct gtc ctc aaa gct cca gtc ccc aaa agg caa aaa tgt gac	310
48	Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg Gln Lys Cys Asp	
49	50 55 60	
51	cac tgg act ccc tgc cca tct gac acc tat gcc tac agg tta ctc agc	358
52	His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala Tyr Arg Leu Leu Ser	
53	65 70 75 80	
55	gga ggt ggc aga agc aag tac gcc aaa atc tgc ttt gag gat aac cta	406
56	Gly Gly Gly Arg Ser Lys Tyr Ala Lys Ile Cys Phe Glu Asp Asn Leu	
57	85 90 95	
59	ctt atg gga gaa cag ctg gga aat gtt gcc aga gga ata aac att gcc	454
60	Leu Met Gly Glu Gln Leu Gly Asn Val Ala Arg Gly Ile Asn Ile Ala	
61	100 105 110	

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```

63 att gtc aac tat gta act ggg aat gtg aca gca aca cga tgt ttt gat 502
64 Ile Val Asn Tyr Val Thr Gly Asn Val Thr Ala Thr Arg Cys Phe Asp
65 115 120 125
67 atg tat gaa ggc gat aac tct gga ccg atg aca aag ttt att cag agt 550
68 Met Tyr Glu Gly Asp Asn Ser Gly Pro Met Thr Lys Phe Ile Gln Ser
69 130 135 140
71 gct gct cca aaa tcc ctg ctc ttc atg gtg acc tat gac gac gga agc 598
72 Ala Ala Pro Lys Ser Leu Leu Phe Met Val Thr Tyr Asp Asp Gly Ser
73 145 150 155 160
75 aca aga ctg aat aac gat gcc aag aat gcc ata gaa gca ctt gga agt 646
76 Thr Arg Leu Asn Asn Asp Ala Lys Asn Ala Ile Glu Ala Leu Gly Ser
77 165 170 175
79 aaa gaa atc agg aac atg aaa ttc agg tct agc tgg gta ttt att gca 694
80 Lys Glu Ile Arg Asn Met Lys Phe Arg Ser Ser Trp Val Phe Ile Ala
81 180 185 190
83 gca aaa ggc ttg gaa ctc cct tcc gaa att cag aga gaa aag atc aac 742
84 Ala Lys Gly Leu Glu Leu Pro Ser Glu Ile Gln Arg Glu Lys Ile Asn
85 195 200 205
87 cac tct gat gct aag aac aac aga tat tct ggc tgg cct gca gag atc 790
88 His Ser Asp Ala Lys Asn Asn Arg Tyr Ser Gly Trp Pro Ala Glu Ile
89 210 215 220
91 cag ata gaa ggc tgc ata ccc aaa gaa cga agc tgacactgca gggctcctgag 843
92 Gln Ile Glu Gly Cys Ile Pro Lys Glu Arg Ser
93 225 230 235
95 taaatgtgtt ctgtataaac aaatgcagct gga 876
97 <210> SEQ ID NO: 2
98 <211> LENGTH: 235
99 <212> TYPE: PRT
100 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 2
103 Met Arg Pro Leu Ala Gly Gly Leu Leu Lys Val Val Phe Val Val Phe
104 1 5 10 15
105 Ala Ser Leu Cys Ala Trp Tyr Ser Gly Tyr Leu Leu Ala Glu Leu Ile
106 20 25 30
107 Pro Asp Ala Pro Leu Ser Ser Ala Ala Tyr Ser Ile Arg Ser Ile Gly
108 35 40 45
109 Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg Gln Lys Cys Asp
110 50 55 60
111 His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala Tyr Arg Leu Leu Ser
112 65 70 75 80
113 Gly Gly Gly Arg Ser Lys Tyr Ala Lys Ile Cys Phe Glu Asp Asn Leu
114 85 90 95
115 Leu Met Gly Glu Gln Leu Gly Asn Val Ala Arg Gly Ile Asn Ile Ala
116 100 105 110
117 Ile Val Asn Tyr Val Thr Gly Asn Val Thr Ala Thr Arg Cys Phe Asp
118 115 120 125
119 Met Tyr Glu Gly Asp Asn Ser Gly Pro Met Thr Lys Phe Ile Gln Ser
120 130 135 140
121 Ala Ala Pro Lys Ser Leu Leu Phe Met Val Thr Tyr Asp Asp Gly Ser

```

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```

122 145          150          155          160
123 Thr Arg Leu Asn Asn Asp Ala Lys Asn Ala Ile Glu Ala Leu Gly Ser
124          165          170          175
125 Lys Glu Ile Arg Asn Met Lys Phe Arg Ser Ser Trp Val Phe Ile Ala
126          180          185          190
127 Ala Lys Gly Leu Glu Leu Pro Ser Glu Ile Gln Arg Glu Lys Ile Asn
128          195          200          205
129 His Ser Asp Ala Lys Asn Asn Arg Tyr Ser Gly Trp Pro Ala Glu Ile
130          210          215          220
131 Gln Ile Glu Gly Cys Ile Pro Lys Glu Arg Ser
132 225          230          235
134 <210> SEQ ID NO: 3
135 <211> LENGTH: 3
136 <212> TYPE: PRT
137 <213> ORGANISM: Artificial Sequence
139 <220> FEATURE:
140 <223> OTHER INFORMATION: Motif 1, corresponding to residues 127 to 129 of
141     SEQ ID NO:2
143 <400> SEQUENCE: 3
144   Phe Asp Met
145     1
147 <210> SEQ ID NO: 4
148 <211> LENGTH: 3
149 <212> TYPE: PRT
150 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <223> OTHER INFORMATION: Motif 2, corresponding to residues 156 to 158 of
154     SEQ ID NO:2
156 <400> SEQUENCE: 4
157   Tyr Asp Asp
158     1
160 <210> SEQ ID NO: 5
161 <211> LENGTH: 3
162 <212> TYPE: PRT
163 <213> ORGANISM: Artificial Sequence
165 <220> FEATURE:
166 <223> OTHER INFORMATION: Motif 3, corresponding to residues 174 to 176 of
167     SEQ ID NO:2
169 <400> SEQUENCE: 5
170   Leu Gly Ser
171     1
173 <210> SEQ ID NO: 6
174 <211> LENGTH: 3
175 <212> TYPE: PRT
176 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE:
179 <223> OTHER INFORMATION: Motif 4, corresponding to residues 188 to 190 of
180     SEQ ID NO:2
182 <400> SEQUENCE: 6

```

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Input Set : A:\97-63C1 SEQ.txt

Output Set: N:\CRF3\05212002\J039876A.raw

```

183 Trp Val Phe
184 1
186 <210> SEQ ID NO: 7
187 <211> LENGTH: 3
188 <212> TYPE: PRT
189 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE:
192 <223> OTHER INFORMATION: Motif 5, corresponding to residues 227 to 229 of
193 SEQ ID NO:2
195 <400> SEQUENCE: 7
196 Glu Gly Cys
197 1
199 <210> SEQ ID NO: 8
200 <211> LENGTH: 705
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence
204 <220> FEATURE:
205 <223> OTHER INFORMATION: z219a Degenerate polynucleotide sequence
W--> 207 <221> NAME/KEY: variation
208 <222> LOCATION: (1)...(705)
209 <223> OTHER INFORMATION: N is any nucleotide
W--> 211 <221> misc_feature
212 <222> LOCATION: (1)...(705)
213 <223> OTHER INFORMATION: n = A,T,C or G
W--> 215 <400> 8
W--> 216 atgmgnccny tngcnggngg nytnytnaar gtngtnttyg tngtnttygc nwsnytnntyg 60
W--> 217 gcntggtayw snggntayyt nytngcngar ytnathccng aygcncny nwsnwsngcn 120
W--> 218 gcntaywsna thmgwnsnat hggngarmgn ccngtnytna argcncngt nccnaarmgn 180
W--> 219 caraartgyg aycaytgac nccntgyccn wsgayacnt aygcntaymg nytnytnwsn 240
W--> 220 ggnggngggnm gnwsnaarta ygcnaarath tgyttygarg ayaayytnyt natgggngar 300
W--> 221 carytnggna aygtngcnmg nggnathaay athgcnahtg tnaaytaygt nacnggnaay 360
W--> 222 gtnacngcna cnmgntgytt ygayatgtay gargngaya aywsnggncc natgacnaar 420
W--> 223 ttyathcarw sngcngcncc naarwsnytn ytnttyatgg tnacntayga ygayggnwsn 480
W--> 224 acnmgnyttna ayaaygaygc naaraaygcn athgargcny tnggnwsnaa rgarathmgn 540
W--> 225 aayatgaart tymgnwsnws ntgggtntty athgcngcna arggnytna rytncnwsn 600
W--> 226 garathcarm gngaraarat haaycaywsn gaygcnaara ayaaymgnta ywsnggntgg 660
W--> 227 ccngcngara thcarathga rggntgyath ccnaargarm gnwsn 705
229 <210> SEQ ID NO: 9
230 <211> LENGTH: 19
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Oligonucleotide primer ZC695
237 <400> SEQUENCE: 9
238 gatttaggtg acactatag 19
240 <210> SEQ ID NO: 10
241 <211> LENGTH: 26
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/039,876A

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; N Pos. 6,9,12,15,18,21,24,27,33,36,42,45,51,54,57,63,72,75,81,84,87  
Seq#:8; N Pos. 93,99,105,108,111,114,117,120,123,129,135,138,144,150,153  
Seq#:8; N Pos. 156,159,165,168,171,174,180,201,204,210,213,219,225,231,234  
Seq#:8; N Pos. 237,240,243,246,249,252,255,264,288,291,297,306,309,315,318  
Seq#:8; N Pos. 321,324,336,342,351,354,357,363,366,369,372,375,396,405,408  
Seq#:8; N Pos. 411,417,432,435,438,441,447,450,453,462,465,477,480,483,486  
Seq#:8; N Pos. 489,501,510,519,522,525,528,540,555,558,561,567,576,579,585  
Seq#:8; N Pos. 588,594,597,600,612,630,636,648,654,657,663,666,684,693,702  
Seq#:8; N Pos. 705



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1	ECBOX	1

Total number of pages: 1

Remarks:

Order of re-scan issued on .....